

IM-5
SEQUENCE LISTING

<110> Wonderling, Ramani S.
Boroughs, Karen L.

<120> CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

<130> IM-5

<140> not yet assigned
<141> 2001-07-27

<150> 60/223,016
<151> 2000-08-04

<160> 109

<170> PatentIn version 3.1

<210> 1
<211> 514
<212> DNA
<213> Felis catus

<220>
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<222> (114)..(512)
<223>

<220>
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<223> n = unknown at position 470
Xaa = unknown at position 119

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aaaccttcca gatcccttcc tctcttagga aactattgag cacagggata aag atg 116
Met
1
act gct ata cca gta gat gat tgc atc aac ttt gtg gga atg aaa ttt 164
Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys Phe
5 10 15
att gac aat aca ctt tac ttt gta gct gac agt gat gaa aac ctg gaa 212
Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu Glu
20 25 30
aca gat tac ttt ggc aag ctt gaa cat aaa ctc tca atc tta cga aac 260
Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn
35 40 45
ttg aac gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt 308
Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe
50 55 60 65

[illegible]

ttt atc ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta 404
Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val
85 90 95

acc atc tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac 452
Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn
100 105 110

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aaa att att tcc ttt aan gga atg agt cct cct gag agt atc aat gat      500
Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn Asp
      115                      120                      125

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gaa gga aat gac at 514
Glu Gly Asn Asp
130

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<210> 2
<211> 133
<212> PRT
<213> Felis catus
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<221>  misc_feature
<222>  (119)..(119)
<223>  The 'Xaa' at location 119 stands for Lys, or Asn.
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<220>
<221> misc_feature
<222> (470)..(470)
<223> n = unknown at position 470
      Xaa = unknown at position 119
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1 5 10 15

Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu
20 25 30

Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg
35 40 45

Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val
50 55 60

Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr
65 70 75 80

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Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala
85 90 95

Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu
100 105 110

Asn Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn
115 120 125

Asp Glu Gly Asn Asp
130

<210> 3
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<213> Felis catus

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<222> (45)..(45)
<223> n = unknown at position 45

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cctctagtga ggctatcttt atacatatat atgataaatt cagtccgggg tgcattatct 180
gtacagtcag aatcaggcat atcctcaaac acaggttgat ctccctgggt aatgaagaga 240
acttggtcgt tcaagtttcg taagattgag agtttatggt caagcttgcc aaagtaatct 300
gtttccaggt tttcatcact gtcagctaca aagtaaagtg tattgtcaat aaatttcatt 360
cccacaaagt tgatgcaatc atctactggg atagcagtca tctttatccc tgtgctcaat 420
agtttcctaa gagaggaagg gatctggaag gtttgaggtc cctttctttt cctgagctgt 480
gtagatggca gaaggtggca ggagcgctt tagc 514

<210> 4
<211> 502
<212> DNA
<213> Felis catus

<220>
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<222> (3)..(464)
<223>

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Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln																	
1					5	10						15					
gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat atg cct																	95
Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro																	
					20	25						30					
gat tct gac tgt aca gat aat gca ccc cgg nct gaa ttt atc ata tat																	143
Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr																	
					35	40						45					
atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc tct gtg																	191
Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val																	
					50	55						60					
aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att att tcc																	239
Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser																	
					65	70						75					
ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga aat gac																	287
Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp																	
80					85	90						95					
atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag ata caa																	335
Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln																	
					100	105						110					
ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa aaa gag																	383
Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu																	
					115	120						125					
aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat ggg gat																	431
Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp																	
					130	135						140					
aag tcc ata atg ttc act gtt caa aac aag aat tagatatttaa aattgcataa																	484
Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn																	
					145	150											
tttgaaaaaaaa aaaaaaaaaa																	502

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<220>
<221> misc_feature
<222> (42)..(42)
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<223> The 'Xaa' at location 42 stands for Thr, Ala, Pro, or Ser.

<220>

<221> misc_feature

<222> (126)..(126)

<223> n = unknown at position 126
Xaa = unknown at position 43

<400> 5

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1 5 10 15

Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp
20 25 30

Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr Met
35 40 45

Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn
50 55 60

Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe
65 70 75 80

Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile
85 90 95

Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe
100 105 110

Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys
115 120 125

Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys
130 135 140

Ser Ile Met Phe Thr Val Gln Asn Lys Asn
145 150

<210> 6

<211> 502

<212> DNA

<213> Felis catus

<220>

<221> misc_feature

<222> (377)..(377)

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<211> 607
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (24)..(599)
<223>
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Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn Tyr Lys Thr Met
 95 100 105

tct act ctc tcc tgt gag aac aaa att att tcc ttt aag gaa atg agt 389
 Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe Lys Glu Met Ser
 110 115 120

cct cct gag agt atc aat gat gaa gga aat gac atc ata ttc ttt cag 437
 Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln
 125 130 135

aga agt gtt cca gga cat gat gat aag ata caa ttt gag tct tca ttg 485
 Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu
 140 145 150

tac aag ggg tac ttt cta gct tgt gaa aaa gag aaa gat ctt ttc aaa 533
 Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys
 155 160 165 170

ctc att ttg aaa aaa aag gat gaa aat ggg gat aag tcc ata atg ttc 581
 Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys Ser Ile Met Phe
 175 180 185

act gtt caa aac aag aat tagatatt 607
 Thr Val Gln Asn Lys Asn
 190

<210> 8
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 <212> PRT
 <213> Felis catus

<400> 8

Met Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys
 1 5 10 15

Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu
 20 25 30

Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg
 35 40 45

Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val
 50 55 60

Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr
 65 70 75 80

Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala
 85 90 95

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Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu
100 105 110

Asn Lys Ile Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn
115 120 125

Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His
130 135 140

Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu
145 150 155 160

Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys
165 170 175

Asp Glu Asn Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
180 185 190

<210> 9
<211> 576
<212> DNA
<213> Felis catus

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acactttact ttgtagctga cagtgatgaa aacctggaaa cagattactt tggcaagctt 120
gaacataaac tctcaatctt acgaaacttg aacgaccaag ttctcttcat taaccaggga 180
gatcaacctg tgtttgagga tatgcctgat tctgactgta cagataatgc accccggact 240
gaatttatca tatatatgta taaagatagc ctactagag gtctggcagt aaccatctct 300
gtgaattata agaccatgtc tactctctcc tgtgagaaca aaattatttc ctttaaggaa 360
atgagtcctc ctgagagtat caatgatgaa ggaaatgaca tcatattctt tcagagaagt 420
gttccaggac atgatgataa gatacaattt gagtcttcat tgtacaaggg gtactttcta 480
gcttgtgaaa aagagaaaga tcttttcaaa ctcatcttga aaaaaaagga tgaaaatggg 540
gataagtcca taatgttcac tgttcaaac aagaat 576

<210> 10
<211> 607
<212> DNA
<213> Felis catus

<400> 10
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tacaatgaag	actcaaattg	tatcttatca	tcatgtcctg	gaacacttct	ctgaaagaat	180
atgatgtcat	ttccttcatc	attgatactc	tcaggaggac	tcatttcctt	aaaggaaata	240
attttgttct	cacaggagag	agtagacatg	gtcttataat	tcacagagat	ggttactgcc	300
agacctctag	tgaggctatc	tttatacata	tatatgataa	attcagtcctg	gggtgcatta	360
tctgtacagt	cagaatcagg	catatcctca	aacacagggt	gatctccctg	gttaatgaag	420
agaacttgg	cgttcaagtt	tcgtaagatt	gagagtttat	gttcaagctt	gccaaagtaa	480
tctgtttcca	ggttttcatc	actgtcagct	acaaagtaaa	gtgtattgtc	aataaatttc	540
attcccacaa	agttgatgca	atcatctact	ggtatagcag	tcatctttat	ccctgtgctc	600
aatagtt						607

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1				5					10					15			
gac	caa	ggt	ctc	ttc	att	aac	cag	gga	gat	caa	cct	gtg	ttt	gag	gat		96
Asp	Gln	Val	Leu	Phe	Ile	Asn	Gln	Gly	Asp	Gln	Pro	Val	Phe	Glu	Asp		
			20					25					30				
atg	cct	gat	tct	gac	tgt	aca	gat	aat	gca	ccc	cgg	act	gaa	ttt	atc		144
Met	Pro	Asp	Ser	Asp	Cys	Thr	Asp	Asn	Ala	Pro	Arg	Thr	Glu	Phe	Ile		
			35				40					45					
ata	tat	atg	tat	aaa	gat	agc	ctc	act	aga	ggt	ctg	gca	gta	acc	atc		192
Ile	Tyr	Met	Tyr	Lys	Asp	Ser	Leu	Thr	Arg	Gly	Leu	Ala	Val	Thr	Ile		
	50					55					60						
tct	gtg	aat	tat	aag	acc	atg	tct	act	ctc	tcc	tgt	gag	aac	aaa	att		240
Ser	Val	Asn	Tyr	Lys	Thr	Met	Ser	Thr	Leu	Ser	Cys	Glu	Asn	Lys	Ile		
65					70					75					80		
att	tcc	ttt	aag	gaa	atg	agt	cct	cct	gag	agt	atc	aat	gat	gaa	gga		288
Ile	Ser	Phe	Lys	Glu	Met	Ser	Pro	Pro	Glu	Ser	Ile	Asn	Asp	Glu	Gly		
				85					90					95			
aat	gac	atc	ata	ttc	ttt	cag	aga	agt	gtt	cca	gga	cat	gat	gat	aag		336
Asn	Asp	Ile	Ile	Phe	Phe	Gln	Arg	Ser	Val	Pro	Gly	His	Asp	Asp	Lys		

[illegible]

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100 105 110
 ata caa ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa 384
 Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu
 115 120 125
 aaa gag aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat 432
 Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn
 130 135 140
 ggg gat aag tcc ata atg ttc act gtt caa aac aag aat 471
 Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
 145 150 155
 <210> 12
 <211> 157
 <212> PRT
 <213> Felis catus
 <400> 12
 Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn
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 20 25 30
 Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile
 35 40 45
 Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile
 50 55 60
 Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile
 65 70 75 80
 Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly
 85 90 95
 Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys
 100 105 110
 Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu
 115 120 125
 Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn
 130 135 140
 Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn

145

150

155

<210> 13
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 agactcaaat tgtatcttat catcatgtcc tggaacactt ctctgaaaga atatgatgtc 180
 atttccttca tcattgatac tctcaggagg actcatttcc ttaaaggaaa taattttgtt 240
 ctcacaggag agagtagaca tggctttata attcacagag atgggttactg ccagacctct 300
 agtgaggcta tctttataca tatatatgat aaattcagtc cggggtgcat tatctgtaca 360
 gtcagaatca ggcatactct caaacacagg ttgatctccc tgggttaatga agagaacttg 420
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 1 5 10 15
 gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa 96
 Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
 20 25 30
 aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct 144
 Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
 35 40 45
 acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgg aaa 192
 Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
 50 55 60
 ggg cca cgg gcg tgc cag atc ttt atc tgt cac atc tgt gag gaa gac 240
 Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
 65 70 75 80
 acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga 288

[illegible]

Thr	His	Leu	Ala	Glu	Thr	Leu	Gly	Leu	Ser	Ser	Ser	Pro	Gln	Ser	Gly		
				85					90					95			
aat	tct	cag	aac	acc	acg	gac	tct	gaa	gta	gcg	ttt	cct	cct	ctt	cca	336	
Asn	Ser	Gln	Asn	Thr	Thr	Asp	Ser	Glu	Val	Ala	Phe	Pro	Pro	Leu	Pro		
				100					105					110			
gcc	agc	gtg	aat	aac	atg	cct	ggg	ccg	gct	gag	cca	gaa	gaa	tct	gta	384	
Ala	Ser	Val	Asn	Asn	Met	Pro	Gly	Pro	Ala	Glu	Pro	Glu	Glu	Ser	Val		
				115					120					125			
gat	gct	ctc	aag	ctt	tgt	cct	cgt	gaa	aac	ttc	gtg	aaa	ctg	tgt	aaa	432	
Asp	Ala	Leu	Lys	Leu	Cys	Pro	Arg	Glu	Asn	Phe	Val	Lys	Leu	Cys	Lys		
				130					135					140			
cag	agg	gct	gaa	gag	atc	tac	cca	ata	aag	gag	aga	aag	gat	cgt	act	480	
Gln	Arg	Ala	Glu	Glu	Ile	Tyr	Pro	Ile	Lys	Glu	Arg	Lys	Asp	Arg	Thr		
				145					150					155			
cgt	ctg	gct	ctc	atc	ata	tgc	aat	acg	acg	ttc	gat	cat	ctt	tct	ctc	528	
Arg	Leu	Ala	Leu	Ile	Ile	Cys	Asn	Thr	Thr	Phe	Asp	His	Leu	Ser	Leu		
				165					170					175			
agg	aag	ggg	gct	gac	ctt	gac	gtt	gca	ggg	atg	agg	agg	ctg	ctt	aca	576	
Arg	Lys	Gly	Ala	Asp	Leu	Asp	Val	Ala	Gly	Met	Arg	Arg	Leu	Leu	Thr		
				180					185					190			
gac	ctt	ggc	tac	agt	gtg	cac	ata	aaa	gag	gaa	ctc	act	gct	aag	gac	624	
Asp	Leu	Gly	Tyr	Ser	Val	His	Ile	Lys	Glu	Glu	Leu	Thr	Ala	Lys	Asp		
				195					200					205			
atg	gaa	tca	gag	ctg	agg	gca	ttt	gct	gcc	cgt	cca	gag	cac	aag	tcc	672	
Met	Glu	Ser	Glu	Leu	Arg	Ala	Phe	Ala	Ala	Arg	Pro	Glu	His	Lys	Ser		
				210					215					220			
tcg	gac	agc	aca	ttc	ctg	gtg	ttc	atg	tct	cat	ggc	atc	ctg	agt	gga	720	
Ser	Asp	Ser	Thr	Phe	Leu	Val	Phe	Met	Ser	His	Gly	Ile	Leu	Ser	Gly		
				225					230					235			
atc	tgt	ggg	acg	aag	tac	agc	gct	gaa	gga	gac	cca	gat	gta	ttg	gct	768	
Ile	Cys	Gly	Thr	Lys	Tyr	Ser	Ala	Glu	Gly	Asp	Pro	Asp	Val	Leu	Ala		
				245					250					255			
tat	gac	acc	atc	ttc	cag	att	ttc	aac	aac	cgc	aac	tgc	ctt	agt	cta	816	
Tyr	Asp	Thr	Ile	Phe	Gln	Ile	Phe	Asn	Asn	Arg	Asn	Cys	Leu	Ser	Leu		
				260					265					270			
aag	gac	aag	ccc	aag	gtc	atc	atc	gtc	cag	gcc	tgc	aga	ggg	gaa	aat	864	
Lys	Asp	Lys	Pro	Lys	Val	Ile	Ile	Val	Gln	Ala	Cys	Arg	Gly	Glu	Asn		
				275					280					285			
ttg	ggg	gaa	ctg	ttg	atc	agt	gac	tct	cca	gcg	gcc	cca	atg	gac	agc	912	
Leu	Gly	Glu	Leu	Leu	Ile	Ser	Asp	Ser	Pro	Ala	Ala	Pro	Met	Asp	Ser		
				290					295					300			
act	tca	cag	atg	ggg	agc	agc	ctt	tca	cag	gtg	ggg	gac	aac	cta	gag	960	
Thr	Ser	Gln	Met	Gly	Ser	Ser	Leu	Ser	Gln	Val	Gly	Asp	Asn	Leu	Glu		
				305					310					315			

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Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu
165 170 175

Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr
180 185 190

Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp
195 200 205

Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser
210 215 220

Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly
225 230 235 240

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala
245 250 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu
260 265 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn
275 280 285

Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser
290 295 300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu
305 310 315 320

Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe
325 330 335

Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly
340 345 350

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Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp
 355 360 365

Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu
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Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met
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Thr Arg Cys Phe Tyr Leu Phe Pro Gly His
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 cttgttcacg tctctccaag acacatgatg tggggctcgag gaggagaaag cgatgaagtc 240
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526

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35 40 45

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50 55 60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
65 70 75 80

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr
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 gcatctacag attcttctgg ctacagccggc ccaggcatgt tattcacgct ggctggaaga 180
 ggaggaaacg ctacttcaga gtccgtggtg ttctgagaat ttccagattg tgggcttgag 240
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 aagagttcat ccagcaagcc gttgaccgtc cccatgcoga ctgagttgat gaactgcttc 480
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 Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp
 20 25 30
 gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc tgc 143
 Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys
 35 40 45
 tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga tct 191
 Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser
 50 55 60
 ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg tgc 239
 Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys

IM-5

65 70 75

ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa aaa 287
Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys
80 85 90 95

cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg aca 335
Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr
100 105 110

aga tac ttc tat ctc ttc cct ggc aat tgaaaatagc aatcatgggc 382
Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
115 120

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35 40 45

Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser Leu
50 55 60

Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys Phe
65 70 75 80

His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys Pro
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 ccatgattgc tatttttcaat tgccagggaa gagatagaag tatcttgtca tggatagtcg 180
 ttcaatgggtg ggcattctggg ctctaacatt tggtttttca aatgactggt gtaccttccg 240
 aaataacttcc tccagatgaa agcaccacga atacttttgg aagcacgtga tgagttgtgt 300
 aatgaagaga gatcccttgt tcacgtctct ccaagacaca tgatgtgggg tcgaggagca 360
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 Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys
 20 25 30
 aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct 144
 Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
 35 40 45

IM-5

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Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys	
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Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp	
65 70 75 80	
acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga	288
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly	
85 90 95	
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Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro	
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Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val	
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130 135 140	
cag agg gct gaa gag atc tac cca ata aag gag aga aag gat cgt act	480
Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr	
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165 170 175	
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180 185 190	
gac ctt ggc tac agt gtg cac ata aaa gag gaa ctc act gct aag gac	624
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195 200 205	
atg gaa tca gag ctg agg gca ttt gct gcc cgt cca gag cac aag tcc	672
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210 215 220	
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225 230 235 240	
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245 250 255	
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Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu	
260 265 270	
aag gac aag ccc aag gtc atc atc gtc cag gcc tgc aga ggt gaa aat	864
Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn	
275 280 285	

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act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag 960
 Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu
 305 310 315 320

gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc 1008
 Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe
 325 330 335

tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga 1056
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 340 345 350

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 355 360 365

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 Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu
 370 375 380

aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg 1200
 Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met
 385 390 395 400

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 405 410

<210> 24
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 <213> Felis catus

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20 25 30

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Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
50 55 60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
65 70 75 80

IM-5

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly
 85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro
 100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val
 115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys
 130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr
 145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu
 165 170 175

Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr
 180 185 190

Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp
 195 200 205

Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser
 210 215 220

Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly
 225 230 235 240

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala
 245 250 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu
 260 265 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn
 275 280 285

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IM-5

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130	135	140	
gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg			480
Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val			
145	150	155	160
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt			528
Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser			
165	170	175	
gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac			576
Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp			
180	185	190	
gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc			624
Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile			
195	200	205	
agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca			672
Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro			
210	215	220	
tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc			720
Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr			
225	230	235	240
tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc			768
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val			
245	250	255	
cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag			816
Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys			
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acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa			864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln			
275	280	285	
gcc aga gac cgc tac tat agc tca tcc tgg agc aac tgg gca tcc gtg			912
Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val			
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Ser Gly Lys	Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly		
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Gln Tyr Thr	Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu		
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Leu Ile His	Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg		
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Glu Gln Lys	Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys		
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Asn Tyr Ser	Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr		
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Asp Leu Lys	Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln		
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Glu Val Thr	Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val		
	145	150	155
Asp Asn Arg	Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser		
	165	170	175
Ala Cys Pro	Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp		
	180	185	190
Ala Ile His	Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile		
	195	200	205
Arg Asp Ile	Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro		
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Leu Lys Asn	Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr		
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			240

IM-5
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 65 70 75 80
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 85 90 95
 ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg 336
 Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt 384
 Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125
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 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
 165 170 175
 gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg 576
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 180 185 190

IM-5

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 195 200 205

 att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac 672
 Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
 210 215 220

 acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag 720
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
 225 230 235 240

 aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc 768
 Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
 245 250 255

 tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta 816
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
 260 265 270

 aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac 864
 Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
 275 280 285

 aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat 912
 Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
 290 295 300

 gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg 960
 Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320

 agc aac tgg gca tcc gtg tcc tgc agt 987
 Ser Asn Trp Ala Ser Val Ser Cys Ser
 325

<210> 30
 <211> 329
 <212> PRT
 <213> Felis catus

<400> 30

Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
1 5 10 15

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp

290

295

300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
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Ser Asn Trp Ala Ser Val Ser Cys Ser
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 <213> Felis catus

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 tctgtctttc ttttctctgt tgttcttgcc ctggacctgt acgccaaatg ttaaggagaa 180
 gtaggaatgt ggggtgctcc aggtgtcagg gtattcccag ctcaactcca catgccgaga 240
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 gaagaagctg ctggtgtagt tttcgtactt gagcttgtga atagcgtcca ccacgacttc 360
 aatgggtagg ctctcctcgg cagccgggca ggcactgccc tcttgacact ccactgtgta 420
 cttcttataa tccctgttgt ccactctgac cttctctgct gagagtgtcg ctgctccaca 480
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 ggtatactgg ccagcatctg caaattcttt gacttggatg gtcagagttt taccagagcc 780
 taggacttca ctgctctggt cagaggtcca ggtgatgtca tcttcttcag gagtattgca 840
 ggtgaggacc accatttctc cgggggcatc agggtgccag tccaactcta caacataaac 900
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 <212> DNA
 <213> Felis catus

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<222> (1)..(666)

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1 5 10 15	
aac cac ctg gac cac ctc agt ttg gcc agg aac ctc ccc aca ccc aca	96
Asn His Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Thr Pro Thr	
20 25 30	
cca agc cca gga atg ttc cag tgc ctc aac cac tcc caa acc ctg ctg	144
Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu	
35 40 45	
cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa ttt	192
Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe	
50 55 60	
tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa gat	240
Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp	
65 70 75 80	
aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat	288
Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn	
85 90 95	
gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg agt	336
Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser	
100 105 110	
tgc ctg gcc tcc aga aag acc tct ttt atg acg acc ctg tgc ctt agc	384
Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser	
115 120 125	
agt atc tat gag gac ttg aag atg tac cag gtg gag ttc aag gcc atg	432
Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met	
130 135 140	
aat gca aag ctg tta atg gat cct aaa agg cag atc ttt ctg gat caa	480
Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln	
145 150 155 160	
aac atg ctg aca gct att gat gag ctg tta cag gcc ctg aat gtc aac	528
Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn	
165 170 175	
agt gtg act gtg cca cag aac tcc tcc ctg gaa gaa ccg gat ttt tat	576
Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr	
180 185 190	
aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt	624
Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg	
195 200 205	
gca gtg acc atc aat aga atg atg agc tat ctg aat gct tcc	666
Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser	

210

215

220

<210> 33
 <211> 222
 <212> PRT
 <213> Felis catus

<400> 33

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 20 25 30

Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu
 35 40 45

Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe
 50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
 65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
 85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
 100 105 110

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser
 115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met
 130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
 145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn
 165 170 175

Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr
 180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg

[illegible]

IM-5

Ala	Arg	Gln	Thr	Leu	Glu	Phe	Tyr	Ser	Cys	Thr	Ser	Glu	Glu	Ile	Asp		
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cat	gaa	gat	atc	aca	aaa	gat	aaa	acc	agc	aca	gtg	gag	gcc	tgc	tta	192	
His	Glu	Asp	Ile	Thr	Lys	Asp	Lys	Thr	Ser	Thr	Val	Glu	Ala	Cys	Leu		
	50					55					60						
cca	ctg	gaa	tta	acc	atg	aat	gag	agt	tgc	ctg	gct	tcc	aga	gag	atc	240	
Pro	Leu	Glu	Leu	Thr	Met	Asn	Glu	Ser	Cys	Leu	Ala	Ser	Arg	Glu	Ile		
	65				70					75					80		
tct	ctg	ata	act	aat	ggg	agt	tgc	ctg	gcc	tcc	aga	aag	acc	tct	ttt	288	
Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala	Ser	Arg	Lys	Thr	Ser	Phe		
				85					90					95			
atg	acg	acc	ctg	tgc	ctt	agc	agt	atc	tat	gag	gac	ttg	aag	atg	tac	336	
Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser	Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr		
			100					105						110			
cag	gtg	gag	ttc	aag	gcc	atg	aat	gca	aag	ctg	tta	atg	gat	cct	aaa	384	
Gln	Val	Glu	Phe	Lys	Ala	Met	Asn	Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys		
		115					120						125				
agg	cag	atc	ttt	ctg	gat	caa	aac	atg	ctg	aca	gct	att	gat	gag	ctg	432	
Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu	Thr	Ala	Ile	Asp	Glu	Leu		
		130				135					140						
tta	cag	gcc	ctg	aat	gtc	aac	agt	gtg	act	gtg	cca	cag	aac	tcc	tcc	480	
Leu	Gln	Ala	Leu	Asn	Val	Asn	Ser	Val	Thr	Val	Pro	Gln	Asn	Ser	Ser		
					145					155					160		
ttg	gaa	gaa	ccg	gat	ttt	tat	aaa	act	aaa	atc	aag	ctc	tgc	ata	ctt	528	
Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu		
				165					170					175			
ctt	cat	gct	ttc	aga	att	cgt	gca	gtg	acc	atc	aat	aga	atg	atg	agc	576	
Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr	Ile	Asn	Arg	Met	Met	Ser		
			180					185						190			
tat	ctg	aat	gct	tcc												591	
Tyr	Leu	Asn	Ala	Ser													
				195													

<210> 36

<211> 197

<212> PRT

<213> Felis catus

<400> 36

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Asn	His	Ser	Gln	Thr	Leu	Leu	Arg	Ala	Ile	Ser	Asn	Thr	Leu	Gln	Lys
			20					25					30		

IM-5

Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp
35 40 45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
50 55 60

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
65 70 75 80

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
85 90 95

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
100 105 110

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
130 135 140

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
145 150 155 160

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
165 170 175

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
180 185 190

Tyr Leu Asn Ala Ser
195

<210> 37

<211> 591

<212> DNA

<213> Felis catus

<400> 37

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aagaagtatg cagagcttga ttttagtttt ataaaaatcc gggtcttcca aggaggagtt 120

ctgtggcaca gtcacactgt tgacattcag ggctgtaac agctcatcaa tagctgtcag 180

catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240

cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300

[illegible]

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<210> 38
<211> 1599
<212> DNA
<213> Felis catus
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<220>
<221> CDS
<222> (1) .. (1599)
<223>
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IM-5

ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg 145 150 155 160	480
ggc tcc tct gac ccc caa gag gtg act tgt gga gca gcg aca ctc tca Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser 165 170 175	528
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val 180 185 190	576
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro 195 200 205	624
att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210 215 220	672
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys 225 230 235 240	720
aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245 250 255	768
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260 265 270	816
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp 275 280 285	864
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp 290 295 300	912
gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp 305 310 315 320	960
agc aac tgg gca tcc gtg tcc tgc agt ggt ggc ggt ggc ggc gga tct Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser 325 330 335	1008
aga aac ttg cca acc cct act cca tcc ccg ggg atg ttc cag tgc ctc Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu 340 345 350	1056
aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys 355 360 365	1104
gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp	1152

IM-5

370	375	380	
cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta			1200
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu			
385	390	395	400
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc			1248
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile			
	405	410	415
tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt			1296
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe			
	420	425	430
atg acg acc ctg tgc ctt agc agt atc tat gag gac ttg aag atg tac			1344
Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr			
	435	440	445
cag gtg gag ttc aag gcc atg aat gca aag ctg tta atg gat cct aaa			1392
Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys			
	450	455	460
agg cag atc ttt ctg gat caa aac atg ctg aca gct att gat gag ctg			1440
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu			
	465	470	480
tta cag gcc ctg aat gtc aac agt gtg act gtg cca cag aac tcc tcc			1488
Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser			
	485	490	495
ttg gaa gaa ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt			1536
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu			
	500	505	510
ctt cat gct ttc aga att cgt gca gtg acc atc aat aga atg atg agc			1584
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser			
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tat ctg aat gct tcc			1599
Tyr Leu Asn Ala Ser			
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<210> 39

<211> 533

<212> PRT

<213> Felis catus

<400> 39

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			20					25					30		

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu

35	40	45
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln		
50	55	60
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys		
65	70	75
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val		
	85	90
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp		
	100	105
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe		
	115	120
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp		
	130	135
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg		
	145	150
Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser		
	165	170
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val		
	180	185
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro		
	195	200
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr		
	210	215
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys		
	225	230
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser		
	245	250
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu		
	260	265
		270

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Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
 275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
 290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser
 325 330 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
 340 345 350

Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys
 355 360 365

Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp
 370 375 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
 385 390 395 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
 405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe
 420 425 430

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
 435 440 445

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
 450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
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Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser
 485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
 500 505 510

IM-5

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
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Tyr Leu Asn Ala Ser
 530

<210> 40

<211> 1599

<212> DNA

<213> Felis catus

<400> 40

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 ctgtggcaca gtcacactgt tgacattcag ggctgtaac agctcatcaa tagctgtcag 180
 catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240
 cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300
 cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctctct 360
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 gatgtccctg atgaagaagc tgctggtgta gttttcgtac ttgagcttgt gaatagcgtc 960
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 tttcaaactg gtactgattg ccgtcagcca ccagcaggtg aaacgtccag aataattctt 1200
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IM-5

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225					230					235					240	

NAME	ADDRESS	CITY	STATE	ZIP
Mr. J. B. Smith	123 Main St.	Springfield	Ill.	62760
Mr. R. L. Jones	456 Oak Ave.	Chicago	Ill.	60601
Mr. T. E. White	789 Elm St.	Peoria	Ill.	61602
Mr. W. H. Black	101 Maple Dr.	Rockford	Ill.	61101
Mr. C. D. Green	202 Pine St.	Decatur	Ill.	62521
Mr. F. G. Brown	303 Cedar Ave.	Normal	Ill.	62450
Mr. H. I. Blue	404 Birch St.	Urbana	Ill.	61502
Mr. J. K. Red	505 Walnut Dr.	Champaign	Ill.	61820
Mr. L. M. Purple	606 Spruce Ave.	Macomb	Ill.	61455
Mr. N. O. Yellow	707 Ash St.	Normal	Ill.	62450
Mr. P. Q. Grey	808 Hickory Dr.	Urbana	Ill.	61502
Mr. R. S. White	909 Maple Ave.	Champaign	Ill.	61820
Mr. T. U. Black	1010 Oak St.	Macomb	Ill.	61455
Mr. V. W. Green	1111 Pine Dr.	Normal	Ill.	62450
Mr. X. Y. Blue	1212 Cedar Ave.	Urbana	Ill.	61502
Mr. Z. A. Red	1313 Birch St.	Champaign	Ill.	61820
Mr. B. C. Purple	1414 Walnut Dr.	Macomb	Ill.	61455
Mr. D. E. Yellow	1515 Spruce Ave.	Normal	Ill.	62450
Mr. F. G. Grey	1616 Ash St.	Urbana	Ill.	61502
Mr. H. I. White	1717 Hickory Dr.	Champaign	Ill.	61820
Mr. J. K. Black	1818 Maple Ave.	Macomb	Ill.	61455
Mr. L. M. Green	1919 Oak St.	Normal	Ill.	62450
Mr. N. O. Blue	2020 Pine Dr.	Urbana	Ill.	61502
Mr. P. Q. Red	2121 Cedar Ave.	Champaign	Ill.	61820
Mr. R. S. Purple	2222 Birch St.	Macomb	Ill.	61455
Mr. T. U. Yellow	2323 Walnut Dr.	Normal	Ill.	62450
Mr. V. W. Grey	2424 Spruce Ave.	Urbana	Ill.	61502
Mr. X. Y. White	2525 Ash St.	Champaign	Ill.	61820
Mr. Z. A. Black	2626 Hickory Dr.	Macomb	Ill.	61455
Mr. B. C. Green	2727 Maple Ave.	Normal	Ill.	62450
Mr. D. E. Blue	2828 Oak St.	Urbana	Ill.	61502
Mr. F. G. Red	2929 Pine Dr.	Champaign	Ill.	61820
Mr. H. I. Purple	3030 Cedar Ave.	Macomb	Ill.	61455
Mr. J. K. Yellow	3131 Birch St.	Normal	Ill.	62450
Mr. L. M. Grey	3232 Walnut Dr.	Urbana	Ill.	61502
Mr. N. O. White	3333 Spruce Ave.	Champaign	Ill.	61820
Mr. P. Q. Black	3434 Ash St.	Macomb	Ill.	61455
Mr. R. S. Green	3535 Hickory Dr.	Normal	Ill.	62450
Mr. T. U. Blue	3636 Maple Ave.	Urbana	Ill.	61502
Mr. V. W. Red	3737 Oak St.	Champaign	Ill.	61820
Mr. X. Y. Purple	3838 Pine Dr.	Macomb	Ill.	61455
Mr. Z. A. Yellow	3939 Cedar Ave.	Normal	Ill.	62450
Mr. B. C. Grey	4040 Birch St.	Urbana	Ill.	61502
Mr. D. E. White	4141 Walnut Dr.	Champaign	Ill.	61820
Mr. F. G. Black	4242 Spruce Ave.	Macomb	Ill.	61455
Mr. H. I. Green	4343 Ash St.	Normal	Ill.	62450
Mr. J. K. Blue	4444 Hickory Dr.	Urbana	Ill.	61502
Mr. L. M. Red	4545 Maple Ave.	Champaign	Ill.	61820
Mr. N. O. Purple	4646 Oak St.	Macomb	Ill.	61455
Mr. P. Q. Yellow	4747 Pine Dr.	Normal	Ill.	62450
Mr. R. S. Grey	4848 Cedar Ave.	Urbana	Ill.	61502
Mr. T. U. White	4949 Birch St.	Champaign	Ill.	61820
Mr. V. W. Black	5050 Walnut Dr.	Macomb	Ill.	61455
Mr. X. Y. Green	5151 Spruce Ave.	Normal	Ill.	62450
Mr. Z. A. Blue	5252 Ash St.	Urbana	Ill.	61502
Mr. B. C. Red	5353 Hickory Dr.	Champaign	Ill.	61820
Mr. D. E. Purple	5454 Maple Ave.	Macomb	Ill.	61455
Mr. F. G. Yellow	5555 Oak St.	Normal	Ill.	62450
Mr. H. I. Grey	5656 Pine Dr.	Urbana	Ill.	61502
Mr. J. K. White	5757 Cedar Ave.	Champaign	Ill.	61820
Mr. L. M. Black	5858 Birch St.	Macomb	Ill.	61455
Mr. N. O. Green	5959 Walnut Dr.	Normal	Ill.	62450
Mr. P. Q. Blue	6060 Spruce Ave.	Urbana	Ill.	61502
Mr. R. S. Red	6161 Ash St.	Champaign	Ill.	61820
Mr. T. U. Purple	6262 Hickory Dr.	Macomb	Ill.	61455
Mr. V. W. Yellow	6363 Maple Ave.	Normal	Ill.	62450
Mr. X. Y. Grey	6464 Oak St.	Urbana	Ill.	61502
Mr. Z. A. White	6565 Pine Dr.	Champaign	Ill.	61820
Mr. B. C. Black	6666 Cedar Ave.	Macomb	Ill.	61455
Mr. D. E. Green	6767 Birch St.	Normal		

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IM-5

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IM-5

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THE
NEW
YORK
PUBLIC
LIBRARY

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IM-5

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Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met
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145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn
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Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
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Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	Thr	Cys	His	Thr	Pro	Glu	
			20					25					30			
gaa	gat	gac	atc	act	tgg	acc	tca	gcg	cag	agc	agt	gaa	gtc	cta	ggt	144
Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Ala	Gln	Ser	Ser	Glu	Val	Leu	Gly	
			35				40					45				
tct	ggt	aaa	act	ctg	acc	atc	caa	gtc	aaa	gaa	ttt	gga	gat	gct	ggc	192
Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	Glu	Phe	Gly	Asp	Ala	Gly	
	50					55					60					
cag	tat	acc	tgc	cat	aaa	gga	ggc	aag	gtt	ctg	agc	cgc	tca	ctc	ctg	240
Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Lys	Val	Leu	Ser	Arg	Ser	Leu	Leu	
65					70				75					80		
ttg	att	cac	aaa	aaa	gaa	gat	gga	att	tgg	tcc	act	gat	atc	tta	aag	288
Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	Ser	Thr	Asp	Ile	Leu	Lys	
				85					90					95		
gaa	cag	aaa	gaa	tcc	aaa	aat	aag	atc	ttt	ctg	aaa	tgt	gag	gca	aag	336
Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	Leu	Lys	Cys	Glu	Ala	Lys	
			100					105					110			
aat	tat	tct	gga	cgt	ttc	aca	tgc	tgg	tgg	ctg	acg	gca	atc	agt	act	384
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Ala	Ile	Ser	Thr	
			115				120					125				
gat	ttg	aaa	ttc	agt	gtc	aaa	agt	agc	aga	ggc	ttc	tct	gac	ccc	caa	432
Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg	Gly	Phe	Ser	Asp	Pro	Gln	
	130					135					140					
ggg	gtg	aca	tgt	gga	gca	gtg	aca	ctt	tca	gca	gag	agg	gtc	aga	gtg	480
Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser	Ala	Glu	Arg	Val	Arg	Val	
145					150					155					160	
gac	aac	agg	gat	tat	aag	aag	tac	aca	gtg	gag	tgt	cag	gag	ggc	agt	528
Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser	
				165				170						175		
gcc	tgc	ccc	tct	gcc	gag	gag	agc	cta	ccc	atc	gag	gtc	gtg	gtg	gat	576
Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp	
			180					185					190			
gct	att	cac	aag	ctc	aag	tat	gaa	aac	tac	acc	agc	agc	ttc	ttc	atc	624
Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile	
			195				200						205			
aga	gac	atc	atc	aaa	cca	gac	cca	ccc	aca	aac	ctg	cag	ctg	aag	cca	672
Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro	
	210					215					220					
ttg	aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	tgg	gaa	tac	ccc	gac	acc	720
Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	
225					230					235					240	

IM-5

tgg agc acc cca cat tcc tac ttc tcc ctg aca ttt tgc ata cag gcc	768
Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala	
245 250 255	
cag ggc aag aac aat aga gaa aag aaa gat aga ctc tgc gtg gac aag	816
Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys	
260 265 270	
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa	864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln	
275 280 285	
gcc cga gac cgc tac tat agt tca tcc tgg agc gac tgg gca tct gtg	912
Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val	
290 295 300	
tcc tgc agt	921
Ser Cys Ser	
305	
<210> 53	
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<212> PRT	
<213> Canis familiaris	
<400> 53	
Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His	
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Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu	
20 25 30	
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly	
35 40 45	
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly	
50 55 60	
Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu	
65 70 75 80	
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys	
85 90 95	
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys	
100 105 110	
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr	
115 120 125	

IM-5

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
145 150 155 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
165 170 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro
210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val
290 295 300

Ser Cys Ser
305

<210> 54
<211> 921
<212> DNA
<213> Canis familiaris

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cacgcggatc ttggcatcct tgtggcacac gaccttggct gaggtcttgt ccacgcagag 120

IM-5

tctatctttc ttttctctat tgttcttgcc ctgggcctgt atgcaaaatg tcaggagagaa 180
 gtaggaatgt ggggtgctcc aggtgtcggg gtattcccag ctgacctcca cgtgccgaga 240
 atttttcaat ggcttcagct gcaggtttgt ggggtgggtct gggttgatga tgtctctgat 300
 gaagaagctg ctgggtgtagt tttcatactt gagcttgtga atagcatcca ccacgacctc 360
 gatgggtagg ctctcctcgg cagaggggca ggcactgccc tcctgacact ccactgtgta 420
 cttcttataa tccctgttgt ccactctgac cctctctgct gaaagtgtca ctgctccaca 480
 tgtcaccctt tgggggtcag agaagcctct gctacttttg acactgaatt tcaaactcagt 540
 actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattctttg cctcacattt 600
 cagaaagatc ttatTTTTTgg attctttctg ttcctttaag atatcagtgg accaaattcc 660
 atcttctttt ttgtgaatca acaggagtga gcggctcaga accttgccctc ctttatggca 720
 ggtatactgg ccagcatctc caaattcttt gacttggatg gtcagagttt taccagaacc 780
 taggacttca ctgctctgcg ctgaggtcca agtgatgtca tcttcttcag gggatatggca 840
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 atctttctcc agttcccata t 921

<210> 55
 <211> 985
 <212> DNA
 <213> Felis catus

<220>
 <221> CDS
 <222> (1)..(984)
 <223>

<400> 55
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 Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
 1 5 10 15
 gca cct ccc ctg atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt 96
 Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
 20 25 30
 gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctg 144
 Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45
 acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag 192
 Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
 50 55 60
 agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa 240
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys

IM-5

65	70					75					80					
gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt	85					90					95					288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val																
ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg	100					105					110					336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp																
tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt	115					120					125					384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe																
cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg	130					135					140					432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp																
ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga	145					150					155					480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg																
ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca	165					170					175					528
Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser																
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg	180					185					190					576
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val																
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc	195					200					205					624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro																
att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac	210					215					220					672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr																
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag	225					230					235					720
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys																
aac ctg caa ctg aag cca tta aaa aat tct ccg cat gtg gaa gtg agc	245					250					255					768
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser																
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta	260					265					270					816
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu																
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac	275					280					285					864
Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp																
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat	290					295					300					912
Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp																
gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg																960

IM-5

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320

agc aac tgg gca tcc gtg tcc tgc a
 Ser Asn Trp Ala Ser Val Ser Cys
 325

985

<210> 56
 <211> 328
 <212> PRT
 <213> Felis catus

<400> 56

Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
 1 5 10 15

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
 20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
 50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
 85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
 145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
 165 170 175

IM-5

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys
325

<210> 57

<211> 985

<212> DNA

<213> Felis catus

<400> 57

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tgtctttctt ttctctgttg ttcttgccct ggacctgtac gccaaatgtt aaggagaagt 180

aggaatgtgg ggtgctccag gtgtcagggt attcccagct cacttccaca tgccgagaat 240

tttttaaatgg cttcagttgc aggttcttg gtgggtccgg tttgatgatg tccctgatga 300

agaagctgct ggtgtagttt tcgtacttga gcttgtgaat agcgtccacc acgacttcaa 360

tgggtaggct ctctcggca gccgggcagg cactgccctc ctgacactcc actgtgtact 420

IM-5

Leu	Ser	Arg	Ser	Leu	Leu	Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	
			100					105					110			
tcc	act	gat	atc	tta	aag	gaa	cag	aaa	gaa	tcc	aaa	aat	aag	atc	ttt	384
Ser	Thr	Asp	Ile	Leu	Lys	Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	
		115					120					125				
ctg	aaa	tgt	gag	gca	aag	aat	tat	tct	gga	cgt	ttc	aca	tgc	tgg	tgg	432
Leu	Lys	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	
	130					135					140					
ctg	acg	gca	atc	agt	act	gat	ttg	aaa	ttc	agt	gtc	aaa	agt	agc	aga	480
Leu	Thr	Ala	Ile	Ser	Thr	Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg	
	145				150					155					160	
ggc	ttc	tct	gac	ccc	caa	ggg	gtg	aca	tgt	gga	gca	gtg	aca	ctt	tca	528
Gly	Phe	Ser	Asp	Pro	Gln	Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser	
				165					170					175		
gca	gag	agg	gtc	aga	gtg	gac	aac	agg	gat	tat	aag	aag	tac	aca	gtg	576
Ala	Glu	Arg	Val	Arg	Val	Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	
			180					185					190			
gag	tgt	cag	gag	ggc	agt	gcc	tgc	ccc	tct	gcc	gag	gag	agc	cta	ccc	624
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	
		195					200					205				
atc	gag	gtc	gtg	gtg	gat	gct	att	cac	aag	ctc	aag	tat	gaa	aac	tac	672
Ile	Glu	Val	Val	Val	Asp	Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	
	210					215					220					
acc	agc	agc	ttc	ttc	atc	aga	gac	atc	atc	aaa	cca	gac	cca	ccc	aca	720
Thr	Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	
	225				230					235					240	
aac	ctg	cag	ctg	aag	cca	ttg	aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	768
Asn	Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	
				245					250					255		
tgg	gaa	tac	ccc	gac	acc	tgg	agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	816
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	
			260					265					270			
aca	ttt	tgc	ata	cag	gcc	cag	ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	864
Thr	Phe	Cys	Ile	Gln	Ala	Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	
		275					280					285				
aga	ctc	tgc	gtg	gac	aag	acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	912
Arg	Leu	Cys	Val	Asp	Lys	Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	
	290					295					300					
gcc	aag	atc	cgc	gtg	caa	gcc	cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	960
Ala	Lys	Ile	Arg	Val	Gln	Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	
	305				310					315					320	
agc	gac	tgg	gca	tct	gtg	tca	tgc	agt								987
Ser	Asp	Trp	Ala	Ser	Val	Ser	Cys	Ser								
				325												

<400> 59

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
195 200 205

IM-5

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 ggtatactgg ccagcatctc caaattcttt gacttggatg gtcagagttt taccagaacc 780
 taggacttca ctgctctgcg ctgaggtcca agtgatgtca tcttcttcag gggatatggca 840
 ggtgaggacc accatttctc cgggggcatc agggtgccag tccaactcta caacataaac 900
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 <212> DNA
 <213> Canis familiaris

<220>
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 <222> (1)..(1599)
 <223>

<400> 61
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 1 5 10 15
 gcg tct ccc ctc atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt 96
 Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
 20 25 30
 gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc 144
 Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45
 acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag 192
 Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
 50 55 60
 agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa 240
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80
 gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt 288
 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
 85 90 95
 ctg agc cgc tca ctc ctg ttg att cac aaa aaa gaa gat gga att tgg 336
 Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 tcc act gat atc tta aag gaa cag aaa gaa tcc aaa aat aag atc ttt 384
 Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125

IM-5

ctg Leu	aaa Lys	tgt Cys	gag Glu	gca Ala	aag Lys	aat Asn	tat Tyr	tct Ser	gga Gly	cgt Arg	ttc Phe	aca Thr	tgc Cys	tgg Trp	tgg Trp	432
130																
ctg Leu	acg Thr	gca Ala	atc Ile	agt Ser	act Thr	gat Asp	ttg Leu	aaa Lys	ttc Phe	agt Ser	gtc Val	aaa Lys	agt Ser	agc Ser	aga Arg	480
145																
ggc Gly	ttc Phe	tct Ser	gac Asp	ccc Pro	caa Gln	ggg Gly	gtg Val	aca Thr	tgt Cys	gga Gly	gca Ala	gtg Val	aca Thr	ctt Leu	tca Ser	528
165																
gca Ala	gag Glu	agg Arg	gtc Val	aga Arg	gtg Val	gac Asp	aac Asn	agg Arg	gat Asp	tat Tyr	aag Lys	aag Lys	tac Tyr	aca Thr	gtg Val	576
180																
gag Glu	tgt Cys	cag Gln	gag Glu	ggc Gly	agt Ser	gcc Ala	tgc Cys	ccc Pro	tct Ser	gcc Ala	gag Glu	gag Glu	agc Ser	cta Leu	ccc Pro	624
195																
atc Ile	gag Glu	gtc Val	gtg Val	gtg Val	gat Asp	gct Ala	att Ile	cac His	aag Lys	ctc Leu	aag Lys	tat Tyr	gaa Glu	aac Asn	tac Tyr	672
210																
acc Thr	agc Ser	agc Ser	ttc Phe	ttc Phe	atc Ile	aga Arg	gac Asp	atc Ile	atc Ile	aaa Lys	cca Pro	gac Asp	cca Pro	ccc Pro	aca Thr	720
225																
aac Asn	ctg Leu	cag Gln	ctg Leu	aag Lys	cca Pro	ttg Leu	aaa Lys	aat Asn	tct Ser	cgg Arg	cac His	gtg Val	gag Glu	gtc Val	agc Ser	768
245																
tgg Trp	gaa Glu	tac Tyr	ccc Pro	gac Asp	acc Thr	tgg Trp	agc Ser	acc Thr	cca Pro	cat His	tcc Ser	tac Tyr	ttc Phe	tcc Ser	ctg Leu	816
260																
aca Thr	ttt Phe	tgc Cys	ata Ile	cag Gln	gcc Ala	cag Gln	ggc Gly	aag Lys	aac Asn	aat Asn	aga Arg	gaa Glu	aag Lys	aaa Lys	gat Asp	864
275																
aga Arg	ctc Leu	tgc Cys	gtg Val	gac Asp	aag Lys	acc Thr	tca Ser	gcc Ala	aag Lys	gtc Val	gtg Val	tgc Cys	cac His	aag Lys	gat Asp	912
290																
gcc Ala	aag Lys	atc Ile	cgc Arg	gtg Val	caa Gln	gcc Ala	cga Arg	gac Asp	cgc Arg	tac Tyr	tat Tyr	agt Ser	tca Ser	tcc Ser	tgg Trp	960
305																
agc Ser	gac Asp	tgg Trp	gca Ala	tct Ser	gtg Val	tca Ser	tgc Cys	agt Ser	ggg Gly	ggc Gly	ggg Gly	ggc Gly	ggc Gly	gga Gly	tct Ser	1008
325																
aga Arg	aac Asn	ttg Leu	cca Pro	acc Thr	cct Pro	act Thr	cca Pro	tcc Ser	ccg Pro	ggg Gly	atg Met	ttc Phe	caa Gln	tgt Cys	ttg Leu	1056
340																
aac Asn	cac His	tcc Ser	caa Gln	acc Thr	ttg Leu	ttg Leu	aga Arg	gcc Ala	gtc Val	agc Ser	aac Asn	acg Thr	ctt Leu	cag Gln	aag Lys	1104
355																

IM-5

gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat 1152
 Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
 370 375 380

cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta 1200
 His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
 385 390 395 400

cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc 1248
 Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
 405 410 415

tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt 1296
 Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
 420 425 430

atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac 1344
 Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
 435 440 445

cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag 1392
 Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
 450 455 460

agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg 1440
 Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
 465 470 475 480

tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc 1488
 Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
 485 490 495

ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt 1536
 Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
 500 505 510

ctt cat gct ttc aga att cgt gcg gtg acc atc aat aga atg atg tcc 1584
 Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
 515 520 525

tac ttg aac tct tcc 1599
 Tyr Leu Asn Ser Ser
 530

<210> 62
 <211> 533
 <212> PRT
 <213> Canis familiaris

<400> 62

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu
 1 5 10 15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val
 20 25 30

IM-5

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
85 90 95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu

00017266-072704

260

265

270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
 275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
 290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp
 305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser
 325 330 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu
 340 345 350

Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys
 355 360 365

Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
 370 375 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
 385 390 395 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
 405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
 420 425 430

Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
 435 440 445

Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
 450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
 465 470 475 480

Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser
 485 490 495

IM-5

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu
500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser
515 520 525

Tyr Leu Asn Ser Ser
530

<210> 63
<211> 1599
<212> DNA
<213> *Canis familiaris*

<400> 63
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aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120
ctgtggcaca gtcacactgt tgaaattcag ggctgtaac agctcatcga tagctgtcag 180
catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300
cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360
ggaagccagg caactctcat tcatgggttaa ttccagtggg aagcaggcct ccactgtgct 420
ggttttatcc tttgtgatat cttcatgatc aatctcttcg gaagtgcagg aatataattc 480
tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcaacaagg tttgggagtg 540
gttcaaacat tggaacatac ccgggggatgg agtaggggtt ggcaagtttc tagatccgcc 600
gccaccgcca ccaactgcat acacagatgc ccagtcgctc caggatgaac tatagtagcg 660
gtctcggggt tgcacgcgga tcttggcatc cttgtggcac acgaccttggt ctgaggtctt 720
gtccacgcag agtctatctt tcttttctct attgttcttg ccctgggcct gtatgcaaaa 780
tgtcagggag aagtaggaat gtgggggtgct ccaggtgtcg gggatttccc agctgacctc 840
cacgtgccga gaatttttca atggcttcag ctgcaggttt gtgggtgggt ctggtttgat 900
gatgtctctg atgaagaagc tgctggtgta gttttcatac ttgagcttgt gaatagcatc 960
caccacgacc tcgatgggta ggctctcctc ggagagggg caggcactgc cctoctgaca 1020
ctccactgtg tactttcttat aatccctgtt gtccactctg accctctctg ctgaaagtgt 1080
cactgctcca catgtcaccc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140
tttcaaataca gtactgattg ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200
tgccacacat ttcagaaaga tcttattttt ggattctttt tgttccttta agatatcagt 1260

IM-5

ggaccaaatt ccattcttctt ttttgtgaat caacaggagt gagcgggtca gaaccttgcc 1320
 tccttttatgg caggtatact ggccagcatc tccaaattct ttgacttgga tggtcagagt 1380
 tttaccagaa ctaggactt cactgctctg cgctgaggtc caagtgatgt catcttcttc 1440
 aggggtatgg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500
 tacaacataa acatctttct ccagttccca tatggccatg aggggagacg ccagcaaac 1560
 gagggaaaac caggagatga ccaactgctg aggggtgcat 1599

<210> 64
 <211> 0
 <212> DNA
 <213> Canis familiaris

<400> 64
 000

<210> 65
 <211> 0
 <212> DNA
 <213> Canis familiaris

<400> 65
 000

<210> 66
 <211> 1533
 <212> DNA
 <213> Canis familiaris

<220>
 <221> CDS
 <222> (1)..(1533)
 <223>

<400> 66
 ata tgg gaa ctg gag aaa gat gtt tat gtt gta gag ttg gac tgg cac 48
 Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His
 1 5 10 15
 cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa 96
 Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu
 20 25 30
 gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt 144
 Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
 35 40 45
 tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc 192
 Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
 50 55 60
 cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg 240

IM-5

Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Lys	Val	Leu	Ser	Arg	Ser	Leu	Leu		
65					70					75					80		
ttg	att	cac	aaa	aaa	gaa	gat	gga	att	tgg	tcc	act	gat	atc	tta	aag	288	
Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	Ser	Thr	Asp	Ile	Leu	Lys		
				85					90					95			
gaa	cag	aaa	gaa	tcc	aaa	aat	aag	atc	ttt	ctg	aaa	tgt	gag	gca	aag	336	
Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	Leu	Lys	Cys	Glu	Ala	Lys		
			100					105					110				
aat	tat	tct	gga	cgt	ttc	aca	tgc	tgg	tgg	ctg	acg	gca	atc	agt	act	384	
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Ala	Ile	Ser	Thr		
		115					120					125					
gat	ttg	aaa	ttc	agt	gtc	aaa	agt	agc	aga	ggc	ttc	tct	gac	ccc	caa	432	
Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg	Gly	Phe	Ser	Asp	Pro	Gln		
	130					135					140						
ggg	gtg	aca	tgt	gga	gca	gtg	aca	ctt	tca	gca	gag	agg	gtc	aga	gtg	480	
Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser	Ala	Glu	Arg	Val	Arg	Val		
	145				150					155					160		
gac	aac	agg	gat	tat	aag	aag	tac	aca	gtg	gag	tgt	cag	gag	ggc	agt	528	
Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser		
				165					170					175			
gcc	tgc	ccc	tct	gcc	gag	gag	agc	cta	ccc	atc	gag	gtc	gtg	gtg	gat	576	
Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp		
			180					185					190				
gct	att	cac	aag	ctc	aag	tat	gaa	aac	tac	acc	agc	agc	ttc	ttc	atc	624	
Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile		
		195					200					205					
aga	gac	atc	atc	aaa	cca	gac	cca	ccc	aca	aac	ctg	cag	ctg	aag	cca	672	
Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro		
	210					215					220						
ttg	aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	tgg	gaa	tac	ccc	gac	acc	720	
Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr		
	225				230					235				240			
tgg	agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	aca	ttt	tgc	ata	cag	gcc	768	
Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala		
				245					250					255			
cag	ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	aga	ctc	tgc	gtg	gac	aag	816	
Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys		
			260					265					270				
acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	864	
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln		
		275					280					285					
gcc	cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	agc	gac	tgg	gca	tct	gtg	912	
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val		
	290					295					300						

IM-5

Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu
20 25 30

Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly
35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly
50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu
65 70 75 80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys
85 90 95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys
100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr
115 120 125

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln
130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val
145 150 155 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser
165 170 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp
180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile
195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro
210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr
225 230 235 240

IM-5

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val
290 295 300

Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro
305 310 315 320

Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu
325 330 335

Leu Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu
340 345 350

Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys
355 360 365

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met
370 375 380

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly
385 390 395 400

Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu
405 410 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala
420 425 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp
435 440 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe
450 455 460

Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe

465 IM-5 475 480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile
485 490 495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser
500 505 510

<210> 68
<211> 1533
<212> DNA
<213> Canis familiaris

<400> 68
ggaagagttc aagtaggaca tcattctatt gatggtcacc gcacgaattc tgaaagcatg 60
aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120
ctgtggcaca gtcacactgt tgaaattcag ggctgtaac agctcatcga tagctgtcag 180
catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300
cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360
ggaagccagg caactctcat tcatgggttaa ttccagtggg aagcaggcct cactgtgct 420
ggttttatcc tttgtgatat ctcatgatc aatctcttcg gaagtgcagg aatataattc 480
tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcaacaagg tttgggagtg 540
gttcaaacat tggaacatac ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600
gccaccgcca cactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg 660
gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720
gtccacgcag agtctatctt tcttttctct attgttcttg ccctgggcct gtatgcaaaa 780
tgtcagggag aagtaggaat gtggggtgct ccaggtgtcg gggatttccc agctgacctc 840
cacgtgccga gaatttttca atggcttcag ctgcaggttt gtgggtgggt ctggtttgat 900
gatgtctctg atgaagaagc tgctggtgta gttttcatac ttgagcttgt gaatagcatc 960
caccacgacc tcgatgggta ggctctctc ggagagggg caggcactgc cctcctgaca 1020
ctccactgtg tacttcttat aatccctgtt gtccactctg accctctctg ctgaaagtgt 1080
cactgtcca catgtcacc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140
tttcaaataca gtactgattg ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200
tgctcacat ttcagaaaga tcttattttt ggattcttct tgttccttta agatatcagt 1260

IM-5
 ggaccaaatt ccattcttctt ttttgtgaat caacaggagt gagcgggtca gaaccttgcc 1320
 tcctttatgg caggtatact ggccagcatc tccaaattct ttgacttgga tggtcagagt 1380
 ttaccagaa ctaggactt cactgctctg cgctgaggtc caagtgatgt catcttcttc 1440
 aggggtatgg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500
 tacaacataa acatctttct ccagttccca tat 1533

<210> 69
 <211> 30
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 69
 gccaaagctcg aaattaaccc tcactaaagg 30

<210> 70
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 70
 cgacggccag tgaattgtaa tacgactc 28

<210> 71
 <211> 31
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 71
 agtgatgaag gcctggaatc agattacttt g 31

<210> 72
 <211> 32
 <212> DNA
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<220>
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<400> 72
 atggcctgga acattctctt gaaagaatat ga 32

<210> 73
 <211> 30
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 73
 aactattgag cacagggata aagatgactg 30

 <210> 74
 <211> 33
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 74
 aatatctaatt tcttggttttg aacagtgaac att 33

 <210> 75
 <211> 36
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 75
 tatgccggct actttggcaa gcttgaacat aaactc 36

 <210> 76
 <211> 37
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 76
 ggcctcgagc taattcttgt tttgaacagt gaacatt 37

 <210> 77
 <211> 28
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 77
 atggccgaca aggtcctgaa ggagaaga 28

<210> 83
 <211> 60
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 83
 ctgcagtggg ggcggtggcg gcggatctag aaacttgcca acccctactc catccccggg 60

 <210> 84
 <211> 60
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 84
 cccgggggatg gagtaggggt tggcaagttt ctagatccgc cgccaccgcc accactgcag 60

 <210> 85
 <211> 28
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 85
 atgcatcctc agcagttggt catcgcct 28

 <210> 86
 <211> 25
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 86
 tgcaggacac ggatgcccag ttgct 25

 <210> 87
 <211> 37
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Synthetic Primer

 <400> 87

IM-5
acaggtacca tgcatacctca gcagttggtc atcgcct 37

<210> 88
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 88
ctaactgcag gacacggatg cccag 25

<210> 89
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 89
atgtgcccgc cgcgtggcc 19

<210> 90
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 90
ctaggaagca ttcagatagc tcatcat 27

<210> 91
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 91
tatgacccgg ggatgttcca gtgcctcaac cactcccaa 39

<210> 92
<211> 41
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 92
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<210> 93
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 93
ccatcctggg cctgctaagc 20

<210> 94
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 94
ccatctggta catcttcaag tc 22

<210> 95
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 95
aaaaaaccgg ggtatgttcc aatgtttcaa ccaactccc 38

<210> 96
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

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<210> 97
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 97
cttaaaggaa cagaaagaat cc 22

<210> 98
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> Synthetic Primer

<400> 98
ggtattccca gctgacctc 19

<210> 99
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<220>
<223> Synthetic Primer

<400> 99
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<210> 100
<211> 29
<212> DNA
<213> Artificial sequence

<220>
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<400> 100
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<210> 101
<211> 561
<212> DNA
<213> Felis catus

<220>
<221> CDS
<222> (1)..(561)
<223>

<400> 101
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Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile
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agc aac acg ctt cag aag gcc aga caa act cta gaa ttt tac tcc tgc 96
Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys

35

40

45

Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys
50 55 60

Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala
65 70 75 80

Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr
85 90 95

Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys
100 105 110

Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
115 120 125

Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr
130 135 140

Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
145 150 155 160

Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
165 170 175

Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser
180 185

<210> 103

<211> 561

<212> DNA

<213> Felis catus

<400> 103

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ctgtggcaca gtcacactgt tgacattcag ggctgtaac agtcatcaa tagctgtcag 180

catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240

cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggctcg 300

cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctctct 360

ggaagccagg caactctcat tcatgggttaa ttccagtggg aagcaggcct cactgtgtgt 420

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ggttttatct tttgtgatat cttcatgata aatctcttcg gaagtgcagg agtaaaattc 480
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 gttgaggcac tggaacatcc c 561

<210> 104
 <211> 1455
 <212> DNA
 <213> Canis familiaris

<220>
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 <222> (232)..(897)
 <223>

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 gccaaattata aaaatgtgac cccccgggtc ggcctccac cgcgcctc cctgcccggc 180
 tccgcagtcc gcgtccagcg cccgccgggg tccacgcagc gcccgcccag c atg tgc 237
 Met Cys
 1
 ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta agc cac 285
 Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu Ser His
 5 10 15
 ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca ccg agc 333
 Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser Pro Ser
 20 25 30
 cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg aga gcc 381
 Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu Arg Ala
 35 40 45 50
 gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta tat tcc 429
 Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu Tyr Ser
 55 60 65
 tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat aaa acc 477
 Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr
 70 75 80
 agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt 525
 Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser
 85 90 95
 tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt tgc ctg 573
 Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu
 100 105 110
 gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc agc atc 621
 Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser Ser Ile

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tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg aac gca				669
Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met Asn Ala				
	135	140	145	
aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa aac atg				717
Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met				
	150	155	160	
ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac agt gtg				765
Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn Ser Val				
	165	170	175	
act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat aaa act				813
Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr				
	180	185	190	
aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gcg gtg				861
Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val				
	195	200	205	210
acc atc gat aga atg atg agt tat ctg aat tct tcc taaaaagctg				907
Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser				
	215	220		
aggtctctct cgactttaaa gtcattccta taaaaatgtg aacccaaaag aatttttcat				967
aagatagggg ttaagaacca gggagggggg ggcttgacct ggtcctactt aagctagtag				1027
gataattctc atgcttggtt acattagttg ccactcaa at tttgaaagat gtgactgtta				1087
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aaaaaaaa				1455

<210> 105

<211> 222

<212> PRT

<213> Canis familiaris

<400> 105

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25

30

Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu
 35 40 45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu
 50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp
 65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn
 85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser
 100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser
 115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met
 130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln
 145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn
 165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr
 180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg
 195 200 205

Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser
 210 215 220

<210> 106

<211> 1455

<212> DNA

<213> Canis familiaris

<400> 106

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ctcttcaagg gaggatttct gtggcacagt cacactgttg aaattcaggg cctgtaacag 720
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<210> 107
<211> 2267
<212> DNA
<213> Canis familiaris

<220>
<221> CDS
<222> (154)..(1140)
<223>

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Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile	Arg		
				220					225					230			
gac	atc	atc	aaa	cca	gac	cca	ccc	aca	aac	ctg	cag	ctg	aag	cca	ttg		894
Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro	Leu		
			235					240					245				
aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	tgg	gaa	tac	ccc	gac	acc	tgg		942
Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	Trp		
		250						255				260					
agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	aca	ttt	tgc	ata	cag	gcc	cag		990
Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala	Gln		
	265					270					275						
ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	aga	ctc	tgc	gtg	gac	aag	acc		1038
Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys	Thr		
280					285					290					295		
tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	gcc		1086
Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln	Ala		
				300					305					310			
cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	agc	gac	tgg	gca	tct	gtg	tcc		1134
Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val	Ser		
			315					320					325				
tgc	agt	taggttccac	ccccaggatg	aatcttggag	ggaaagtgga	agatattatg											1190
Cys	Ser																
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tgataaagca	attcagggcc	acttgcattt	ttaagcaagt	ttagtttttg	gatgcctgaa												1790
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<210> 108
 <211> 329
 <212> PRT
 <213> Canis familiaris

<400> 108

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 Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
 35 40 45
 Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln
 50 55 60
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
 65 70 75 80
 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val
 85 90 95
 Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
 100 105 110
 Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
 115 120 125
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
 130 135 140
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg
 145 150 155 160

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Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser
165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu
260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp
275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp
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Ser Asp Trp Ala Ser Val Ser Cys Ser
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<210> 109

<211> 2267

<212> DNA

<213> Canis familiaris

<400> 109

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aatcacttta cagaaagcac attcattact taaaagtagc acctcagcga ttggcacttt 180

ctggtcacat ccaccagtca ggttcacttg cgctgtccag taagcaattc ttgaccattt 240

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